

## SEQUENCE LISTING

A4  
(1) GENERAL INFORMATION

- (i) APPLICANT: Motoharu SEIKI et al.
- (ii) TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
(B) STREET: 2033 K Street, N.W., Suite 800  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: U.S.A.  
(F) ZIP: 20006
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: MS-DOS  
(D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: NEW  
(B) FILING DATE: December 12, 2000  
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/000,041  
(B) FILING DATE: February 20, 1998  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/JP96/01956  
(B) FILING DATE: July 12, 1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Lee Cheng  
(B) REGISTRATION NUMBER: 40,949  
(C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-721-8200  
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(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2116  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

09734003-121200

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GGCTCCTTAC CCACCCGGAG ACTTTTTTTTT GAAAGGAAAC TAGGGAGGGAGGGAGAGGGA      60
GAGAGGGAGA AAACGAAGGG GAGCTCGTCC ATCCATTGAA GCACAGTTCA CT ATG      115
                                     Met
                                     1
ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTG GAT TTC GTG CAT CAT      163
Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His
          5                      10                      15
TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA      211
Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr
          20                      25                      30
GTC TGC GGA ACG GAG CAG TAT TTC AAT GTG GAG GTT TGG TTA CAA AAG      259
Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys
          35                      40                      45
TAC GGC TAC CTT CCA CCG ACT GAC CCC AGA ATG TCA GTG CTG CGC TCT      307
Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg Ser
          50                      55                      60                      65
GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT GGC      355
Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly
          70                      75                      80
ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT GAC TGG ATG AAG      403
Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys
          85                      90                      95
AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT      451
Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe
          100                      105                      110
CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC      499
His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His
          115                      120                      125
AAG CAC ATC ACT TAC AGT ATA AAG AAC GTA ACT CCA AAA GTA GGA GAC      547
Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly Asp
          130                      135                      140                      145
CCT GAG ACT CGT AAA GCT ATT CGC CGT GCC TTT GAT GTG TGG CAG AAT      595
Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln Asn
          150                      155                      160
GTA ACT CCT CTG ACA TTT GAA GAA GTT CCC TAC AGT GAA TTA GAA AAT      643
Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn
          165                      170                      175

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09734002.12.1200

GGC AAA CGT GAT GTG GAT ATA ACC ATT ATT TTT GCA TCT GGT TTC CAT	691
Gly Lys Arg Asp Val Asp Ile Thr Ile Ile Phe Ala Ser Gly Phe His	
180 185 190	
GGG GAC AGC TCT CCC TTT GAT GGA GAG GGA GGA TTT TTG GCA CAT GCC	739
Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His Ala	
195 200 205	
TAC TTC CCT GGA CCA GGA ATT GGA GGA GAT ACC CAT TTT GAC TCA GAT	787
Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser Asp	
210 215 220 225	
GAG CCA TGG ACA CTA GGA AAT CCT AAT CAT GAT GGA AAT GAC TTA TTT	835
Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe	
230 235 240	
CTT GTA GCA GTC CAT GAA CTG GGA CAT GCT CTG GGA TTG GAG CAT TCC	883
Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His Ser	
245 250 255	
AAT GAC CCC ACT GCC ATC ATG GCT CCA TTT TAC CAG TAC ATG GAA ACA	931
Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu Thr	
260 265 270	
GAC AAC TTC AAA CTA CCT AAT GAT GAT TTA CAG GGC ATC CAG AAA ATA	979
Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys Ile	
275 280 285	
TAT GGT CCA CCT GAC AAG ATT CCT CCA CCT ACA AGA CCT CTA CCG ACA	1027
Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro Thr	
290 295 300 305	
GTG CCC CCA CAC CGC TCT ATT CCT CCG GCT GAC CCA AGG AAA AAT GAC	1075
Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn Asp	
310 315 320	
AGG CCA AAA CCT CCT CGG CCT CCA ACC GGC AGA CCC TCC TAT CCC GGA	1123
Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro Gly	
325 330 335	
GCC AAA CCC AAC ATC TGT GAT GGG AAC TTT AAC ACT CTA GCT ATT CTT	1171
Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile Leu	
340 345 350	
CGT CGT GAG ATG TTT GTT TTC AAG GAC CAG TGG TTT TGG CGA GTG AGA	1219
Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val Arg	
355 360 365	
AAC AAC AGG GTG ATG GAT GGA TAC CCA ATG CAA ATT ACT TAC TTC TGG	1267
Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe Trp	
370 375 380 385	
CGG GGC TTG CCT CCT AGT ATC GAT GCA GTT TAT GAA AAT AGC GAC GGG	1315
Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp Gly	
390 395 400	

09734002-1231200

AAT Asn	TTT Phe	GTG Val	TTC Phe	TTT Phe	AAA Lys	GGT Gly	AAC Asn	AAA Lys	TAT Tyr	TGG Trp	GTG Val	TTC Phe	AAG Lys	GAT Asp	ACA Thr	1363
405410415																
ACT Thr	CTT Leu	CAA Gln	CCT Pro	GGT Gly	TAC Tyr	CCT Pro	CAT His	GAC Asp	TTG Leu	ATA Ile	ACC Thr	CTT Leu	GGA Gly	AGT Ser	GGA Gly	1411
420425430																
ATT Ile	CCC Pro	CCT Pro	CAT His	GGT Gly	ATT Ile	GAT Asp	TCA Ser	GCC Ala	ATT Ile	TGG Trp	TGG Trp	GAG Glu	GAC Asp	GTC Val	GGG Gly	1459
435440445																
AAA Lys	ACC Thr	TAT Tyr	TTC Phe	TTC Phe	AAG Lys	GGA Gly	GAC Asp	AGA Arg	TAT Tyr	TGG Trp	AGA Arg	TAT Tyr	AGT Ser	GAA Glu	GAA Glu	1507
450455460																
ATG Met	AAA Lys	ACA Thr	ATG Met	GAC Asp	CCT Pro	GGC Gly	TAT Tyr	CCC Pro	AAG Lys	CCA Pro	ATC Ile	ACA Thr	GTC Val	TGG Trp	AAA Lys	1555
470475480																
GGG Gly	ATC Ile	CCT Pro	GAA Glu	TCT Ser	CCT Pro	CAG Gln	GGA Gly	GCA Ala	TTT Phe	GTA Val	CAC His	AAA Lys	GAA Glu	AAT Asn	GGC Gly	1603
485490495																
TTT Phe	ACG Thr	TAT Tyr	TTC Phe	TAC Tyr	AAA Lys	GGA Gly	AAG Lys	GAG Glu	TAT Tyr	TGG Trp	AAA Lys	TTC Phe	AAC Asn	AAC Asn	CAG Gln	1651
500505510																
ATA Ile	CTC Leu	AAG Lys	GTA Val	GAA Glu	CCT Pro	GGA Gly	CAT His	CCA Pro	AGA Arg	TCC Ser	ATC Ile	CTC Leu	AAG Lys	GAT Asp	TTT Phe	1699
515520525																
ATG Met	GGC Gly	TGT Cys	GAT Asp	GGA Gly	CCA Pro	ACA Thr	GAC Asp	AGA Arg	GTT Val	AAA Lys	GAA Glu	GGA Gly	CAC His	AGC Ser	CCA Pro	1747
530535540545																
CCA Pro	GAT Asp	GAT Asp	GTA Val	GAC Asp	ATT Ile	GTC Val	ATC Ile	AAA Lys	CTG Leu	GAC Asp	AAC Asn	ACA Thr	GCC Ala	AGC Ser	ACT Thr	1795
550555560																
GTG Val	AAA Lys	GCC Ala	ATA Ile	GCT Ala	ATT Ile	GTC Val	ATT Ile	CCC Pro	TGC Cys	ATC Ile	TTG Leu	GCC Ala	TTA Leu	TGC Cys	CTC Leu	1843
565570575																
CTT Leu	GTA Val	TTG Leu	GTT Val	TAC Tyr	ACT Thr	GTG Val	TTC Phe	CAG Gln	TTC Phe	AAG Lys	AGG Arg	AAA Lys	GGA Gly	ACA Thr	CCC Pro	1891
580585590																
CGC Arg	CAC His	ATA Ile	CTG Leu	TAC Tyr	TGT Cys	AAA Lys	CGC Arg	TCT Ser	ATG Met	CAA Gln	GAG Glu	TGG Trp	GTG Val	TGATGTAGG		1942
595600605																
GTTTTTCTTCTTTCTTTCTTTGCAGGAGTTTGTGGTAACTTGAGATTC AAGACAAGAG2002																
CTGTTATGCTGTTTCCTAGCTAGGAGCAGGCTTGTGGCAGCCTGATTCGGGGCTGACCTT2062																
TCAAACCAGAGGGTGTCTGGTCCTGCACATGAGTGGAAATACACTCATGGGGAA2116																

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607  
(B) TYPE: Amino acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Met 1	Ile	Leu	Leu	Thr 5	Phe	Ser	Thr	Gly	Arg 10	Arg	Leu	Asp	Phe	Val 15	His
His	Ser	Gly	Val 20	Phe	Phe	Leu	Gln	Thr 25	Leu	Leu	Trp	Ile	Leu 30	Cys	Ala
Thr	Val	Cys 35	Gly	Thr	Glu	Gln	Tyr 40	Phe	Asn	Val	Glu	Val 45	Trp	Leu	Gln
Lys	Tyr 50	Gly	Tyr	Leu	Pro	Pro 55	Thr	Asp	Pro	Arg	Met 60	Ser	Val	Leu	Arg
Ser 65	Ala	Glu	Thr	Met	Gln 70	Ser	Ala	Leu	Ala	Ala 75	Met	Gln	Gln	Phe	Tyr 80
Gly	Ile	Asn	Met	Thr 85	Gly	Lys	Val	Asp	Arg 90	Asn	Thr	Ile	Asp	Trp 95	Met
Lys	Lys	Pro	Arg 100	Cys	Gly	Val	Pro	Asp 105	Gln	Thr	Arg	Gly	Ser 110	Ser	Lys
Phe	His	Ile 115	Arg	Arg	Lys	Arg	Tyr 120	Ala	Leu	Thr	Gly	Gln 125	Lys	Trp	Gln
His 130	Lys	His	Ile	Thr	Tyr	Ser 135	Ile	Lys	Asn	Val	Thr 140	Pro	Lys	Val	Gly
Asp 145	Pro	Glu	Thr	Arg	Lys 150	Ala	Ile	Arg	Arg	Ala 155	Phe	Asp	Val	Trp	Gln 160
Asn	Val	Thr	Pro	Leu 165	Thr	Phe	Glu	Glu	Val 170	Pro	Tyr	Ser	Glu	Leu 175	Glu
Asn	Gly	Lys	Arg 180	Asp	Val	Asp	Ile	Thr 185	Ile	Ile	Phe	Ala	Ser 190	Gly	Phe
His	Gly	Asp 195	Ser	Ser	Pro	Phe	Asp 200	Gly	Glu	Gly	Gly	Phe 205	Leu	Ala	His
Ala	Tyr	Phe	Pro	Gly	Pro	Gly	Ile	Gly	Gly	Asp	Thr	His	Phe	Asp	Ser

**Q**uestions **A**nswers

210					215					220					
Asp 225	Glu	Pro	Trp	Thr	Leu 230	Gly	Asn	Pro	Asn	His 235	Asp	Gly	Asn	Asp	Leu 240
Phe	Leu	Val	Ala	Val 245	His	Glu	Leu	Gly	His 250	Ala	Leu	Gly	Leu	Glu 255	His
Ser	Asn	Asp	Pro 260	Thr	Ala	Ile	Met	Ala 265	Pro	Phe	Tyr	Gln	Tyr 270	Met	Glu
Thr	Asp	Asn 275	Phe	Lys	Leu	Pro	Asn 280	Asp	Asp	Leu	Gln	Gly 285	Ile	Gln	Lys
Ile	Tyr 290	Gly	Pro	Pro	Asp	Lys 295	Ile	Pro	Pro	Pro	Thr 300	Arg	Pro	Leu	Pro
Thr 305	Val	Pro	Pro	His	Arg 310	Ser	Ile	Pro	Pro	Ala 315	Asp	Pro	Arg	Lys	Asn 320
Asp	Arg	Pro	Lys	Pro 325	Pro	Arg	Pro	Pro	Thr 330	Gly	Arg	Pro	Ser	Tyr 335	Pro
Gly	Ala	Lys	Pro 340	Asn	Ile	Cys	Asp	Gly 345	Asn	Phe	Asn	Thr	Leu 350	Ala	Ile
Leu	Arg	Arg 355	Glu	Met	Phe	Val	Phe 360	Lys	Asp	Gln	Trp	Phe 365	Trp	Arg	Val
Arg	Asn 370	Asn	Arg	Val	Met	Asp 375	Gly	Tyr	Pro	Met	Gln 380	Ile	Thr	Tyr	Phe
Trp 375	Arg	Gly	Leu	Pro	Pro	Ser	Ile	Asp	Ala	Val 395	Tyr	Glu	Asn	Ser	Asp 400
Gly	Asn	Phe	Val	Phe 405	Phe	Lys	Gly	Asn	Lys 410	Tyr	Trp	Val	Phe	Lys 415	Asp
Thr	Thr	Leu 420	Gln	Pro	Gly	Tyr	Pro	His 425	Asp	Leu	Ile	Thr	Leu 430	Gly	Ser
Gly	Ile	Pro 435	Pro	His	Gly	Ile	Asp	Ser	Ala	Ile	Trp	Trp 445	Glu	Asp	Val
Gly	Lys 450	Thr	Tyr	Phe	Phe	Lys	Gly	Asp	Arg	Tyr	Trp 460	Arg	Tyr	Ser	Glu
Glu 465	Met	Lys	Thr	Met	Asp 470	Pro	Gly	Tyr	Pro	Lys 475	Pro	Ile	Thr	Val	Trp 480
Lys	Gly	Ile	Pro	Glu 485	Ser	Pro	Gln	Gly	Ala 490	Phe	Val	His	Lys	Glu 495	Asn
Gly	Phe	Thr	Tyr 500	Phe	Tyr	Lys	Gly	Lys 505	Glu	Tyr	Trp	Lys	Phe	Asn 510	Asn
Gln	Ile	Leu	Lys	Val	Glu	Pro	Gly	His	Pro	Arg	Ser	Ile	Leu	Lys	Asp

515	520	525
Phe Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser		
530	535	540
Pro Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser		
545	550	555
Thr Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys		
	565	570
Leu Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr		
	580	585
Pro Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val		
	595	600
		605

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

SGNVVNGCWG AYATMRTSAT

20

## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid  
Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

YTCRTSNTCR TCRAARTGRR HRTCYYC

27

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14
  - (B) TYPE: Amino acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

05734000-121200

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Thr Arg Gly Ser Ser Lys Phe His Ile Arg Arg Lys Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14  
(B) TYPE: Amino acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn Gly Lys Arg Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18  
(B) TYPE: Amino acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser Ala Glu Thr Met Gln  
1 5 10 15

Ser Ala

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14  
(B) TYPE: Amino acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe Leu  
1 5 10

09734002-121000



## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7  
(B) TYPE: Amino acid  
(D) STRANDEDNESS: Single  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Gly Glu Ala Asp Ile Leu Val  
1 5

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9  
(B) TYPE: Amino acid  
(D) STRANDEDNESS: Single  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gly Asp Ala His Phe Asp Asp Asp Glu  
1 5

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7  
(B) TYPE: Amino acid  
(D) STRANDEDNESS: Single  
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Gly Glu Ala Asp Ile Met Ile  
1 5

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7  
(B) TYPE: Amino acid  
(D) STRANDEDNESS: Single  
(C) TOPOLOGY: Linear

00734002 12.1.000

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Pro Arg Cys Gly Val Pro Asp  
1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu Leu  
1 5 10 15

Val Leu Val Tyr Thr Val Phe Gln Phe  
20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4  
(B) TYPE: Amino Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Arg Xaa Lys Arg  
1

003400-2300